

Exhibit A. Alignment of nucleotide sequences encoding B domains of four G482 related species

The following is provided for informational purposes
(SEQ ID NOs appear in parentheses; asterisks indicate identical bases in each alignment)

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G482   (4)   AGAGAGCAAGACAGGTTCTTGCCGATCGCTAACGTCAGCCGGATCATGAAGAAGGCCCTTG
G485   (6)   CGTGAGCAAGATAGGTTTCTACCGATCGCTAACGTTAGCAGGATCATGAAGAAAGCACTT
G3395  (74)   AGGGAGCAGGACAGGTTCTGCCATCGCCAACATCAGCCGCATCATGAAGAAGGCCGCTG
G481   (2)   AGGGAGCAGGATCGATACCTTCCTATAGCTAATATCAGCAGGATCATGAAGAAAGCGTTG
          * * * * *
G482   (4)   CCCGCCAACGCCAAGATCTCTAAAGATGCCAAAGAGACGATGCGAGGAGTGTGTCTCCGAG
G485   (6)   CCTGCGAACGCCAAAATCTCTAAGGATGCTAAAGAAACGGTTCAAGAGTGTGTATCCGAA
G3395  (74)   CGGGCGAACGCCAAGATCGCCAAGGACGCCAAGGAGACCTGCGAGGAGTGCCTGCTCCGGAG
G481   (2)   CCTCTAATGGTAAGATTGGAAAAGATGCTAAGGATACAGTTCAGGAATGCGTCTCTGAG
          * * * * *
G482   (4)   TTCATCAGCTTCGTCACCGGAGAAGCATCTGATAAGTGTGAGAAGGAGAAGAGGAAGACG
G485   (6)   TTCATAAGTTTCATCACCAGGTGAGGCTTCTGACAAGTGTGAGAGAGAGAAGAGGAAGACA
G3395  (74)   TTCATCTCCTTCGTCACCGAGGCGGAGCGCAAAATGTGAGAAGGAGAAGCGCCAGAGCC
G481   (2)   TTCATCAGCTTCATCACTAGCGAGGCCAGTGATAAGTGTCAAAAAGAGAAAAGGAAAAC
          * * * * *
G482   (4)   ATCAACGGAGACGATTGCTCTGGGCTATGACTACTCTAGGTTTGTAGGATTATGTTGAG
G485   (6)   ATCAACGGTGACGATCTCTTTGGGCGATGACTACGCTAGGGTTTGTAGGACTACGTTGGAG
G3395  (74)   ATCAACGGGGAAGATCTCCTCTTTGCGATGGGTACGCTTGGCTTGTAGGAGTACGTTGAT
G481   (2)   GTGAATGGTGATGATTGTGTGGGCAATGGCAACATTAGGATTTGAGGATTACCTGGAA
          * * * * *
G482   (4)   CCATTGAAAGTTTACTTGCAGAGGTTTAGGGAG
G485   (6)   CCTCTCAAGGTTTATCTGCAAAAGTATAGGGAG
G3395  (74)   CCGTTGAAGATCTATTACACAAGTACAGAGAG
G481   (2)   CCTCTAAAGATATACCTAGCGAGGTACAGGGAG
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Pairwise sequence alignments:

G482 and G485

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G482   (4)   AGAGAGCAAGACAGGTTCTTGCCGATCGCTAACGTCAGCCGGATCATGAAGAAGGCCCTTG
G482   (6)   CGTGAGCAAGATAGGTTTCTACCGATCGCTAACGTTAGCAGGATCATGAAGAAAGCACTT
          * * * * *
G482   (4)   CCCGCCAACGCCAAGATCTCTAAAGATGCCAAAGAGACGATGCGAGGAGTGTGTCTCCGAG
G485   (6)   CCTGCGAACGCCAAAATCTCTAAGGATGCTAAAGAAACGGTTCAAGAGTGTGTATCCGAA
          * * * * *
G482   (4)   TTCATCAGCTTCGTCACCGGAGAAGCATCTGATAAGTGTGAGAAGGAGAAGAGGAAGACG
G485   (6)   TTCATAAGTTTCATCACCAGGTGAGGCTTCTGACAAGTGTGAGAGAGAGAAGAGGAAGACA
          * * * * *
G482   (4)   ATCAACGGAGACGATTGCTCTGGGCTATGACTACTCTAGGTTTGTAGGATTATGTTGAG
G485   (6)   ATCAACGGTGACGATCTCTTTGGGCGATGACTACGCTAGGGTTTGTAGGACTACGTTGGAG
          * * * * *
G482   (4)   CCATTGAAAGTTTACTTGCAGAGGTTTAGGGAG
G485   (6)   CCTCTCAAGGTTTATCTGCAAAAGTATAGGGAG
          * * * * *

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G482 and G3395

G482 (4) AGAGAGCAAGACAGGTTCTTGCCGATCGCTAACGTCAGCCGGATCATGAAGAAGGCCTTG
G3395 (74) AGGGAGCAGGACAGGTTCTTGCCCATCGCCAACATCAGCCGCATCATGAAGAAGCCGTC
* * * * *

G482 (4) CCCGCCAACGCCAAGATCTCTAAAGATGCCAAAGAGACGATGCAGGAGTGTGTCTCCGAG
G3395 (74) CCGGCGAACGGCAAGATCGCCAAGGACGCCAAGGAGACCTGCAGGAGTGCCTCTCGGAG
* * * * *

G482 (4) TTCATCAGCTTCGTCACCGGAGAAGCATCTGATAAGTGTGAGAAGGAGAAGAGGAAAGCG
G3395 (74) TTCATCTCCTTCGTCACCGAGGCGAGCGACAAATGTGAGAAGGAGAAGCGCAAGACC
* * * * *

G482 (4) ATCAACGGAGACGATTGTCTCTGGCTATGACTACTCTAGGTTTTGAGGATTATGTTGAG
G3395 (74) ATCAACGGGGAAGATCTCCTCTTTGCGATGGGTACGCTTGGCTTTGAGGAGTACGTTGAT
* * * * *

G482 (4) CCATTGAAAGTTTACTTGCAGAGGTTTAGGGAG
G3395 (74) CCGTTGAAGATCTATTACACAAGTACAGAGAG
* * * * *

G482 and G481

G482 (4) AGAGAGCAAGACAGGTTCTTGCCGATCGCTAACGTCAGCCGGATCATGAAGAAGGCCTTG
G481 (6) AGGGAGCAGGATCGATACCTTCCCTATAGCTAATATCAGCAGGATCATGAAGAAGCGTTG
* * * * *

G482 (4) CCCGCCAACGCCAAGATCTCTAAAGATGCCAAAGAGACGATGCAGGAGTGTGTCTCCGAG
G481 (6) CCTCCTAATGGTAAGATTGGAAAAGATGCTAAGGATACAGTTTACGGAATGCGTCTCTGAG
* * * * *

G482 (4) TTCATCAGCTTCGTCACCGGAGAAGCATCTGATAAGTGTGAGAAGGAGAAGAGGAAAGCG
G481 (6) TTCATCAGCTTCATCTACTAGCGAGGCCAGTGATAAGTGTCAAAAAGAGAAAAGGAAAAC
* * * * *

G482 (4) ATCAACGGAGACGATTGTCTCTGGCTATGACTACTCTAGGTTTTGAGGATTATGTTGAG
G481 (6) GTGAATGGTGATGATTGTTGTGGGCAATGGCAACATTAGGATTTGAGGATTACCTGGAA
* * * * *

G482 (4) CCATTGAAAGTTTACTTGCAGAGGTTTAGGGAG
G481 (6) CCTCTAAAGATATACCTAGCGAGGTACAGGGAG
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The following is provided for informational purposes and while Applicants believe the listed percentages are correct, Applicants do not attest to the accuracy of the listed percentages.

Percent Identity to the DNA encoding the G482 B domain, determined with Accelrys Gene v. 2.5

GID		%ID (Accelrys)
G482	(4)	100.0
G485	(6)	80.2
G3395	(74)	77.7
G481	(2)	72.2

Percent Identity to the FL G482 protein determined with BLASTp (no. of identical residues / no. residues compared) or Accelrys Gene v. 2.5

GID		% ID (BLASTp)	%ID (Accelrys)
G482	(4)	100% (190/190)	100.0%
G485	(6)	68% (116/169)	73.3%
G3395	(74)	59% (93/157)	54.9%
G481	(2)	69% (91/131)	63.1%